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The draft genome of *Mycobacterium aurum*, a potential model organism for investigating drugs against *Mycobacterium tuberculosis* and *Mycobacterium leprae*

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ABSTRACT

Mycobacterium aurum (*M. aurum*) is an environmental mycobacteria that has previously been used in studies of anti-mycobacterial drugs due to its fast growth rate and low pathogenicity. The *M. aurum* genome has been sequenced and assembled into 46 contigs, with a total length of 6.02 Mb containing 5684 annotated protein-coding genes. A phylogenetic analysis using whole genome alignments positioned *M. aurum* close to *Mycobacterium vaccae* and *Mycobacterium vanbaalenii*, within a clade related to fast-growing mycobacteria. Large-scale genomic rearrangements were identified by comparing the *M. aurum* genome to those of *Mycobacterium tuberculosis* and *Mycobacterium leprae*. *M. aurum* orthologous genes implicated in resistance to anti-tuberculosis drugs in *M. tuberculosis* were observed. The sequence identity at the DNA level varied from 68.6% for *pncA* (pyrazinamide drug-related) to 96.2% for *rrs* (streptomycin, capreomycin). We observed two homologous genes encoding the catalase-peroxidase enzyme (*katG*) that is associated with resistance to isoniazid. Similarly, two *embB* homologues were identified in the *M. aurum* genome. In addition to describing for the first time the genome of *M. aurum*, this work provides a resource to aid the use of *M. aurum* in studies to develop improved drugs for the pathogenic mycobacteria *M. tuberculosis* and *M. leprae*.

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Introduction

Mycobacterium aurum (*M. aurum*) is an acid-fast, gram-positive environmental bacteria typically found in damp conditions [1,2]. It is a fast-growing mycobacterium with an *in vitro* doubling time of 2–3 h that rarely causes infections in humans [2–6]. The *M. aurum* cell wall contains mycolic acids which are analogous to those found in *Mycobacterium tuberculosis* [7], and there are similarities between the antibiotic susceptibility profiles of the two organisms [8,9]. The fast growth rate and low pathogenicity of *M. aurum* have encouraged its use as a surrogate for the highly pathogenic *M. tuberculosis* in studies of anti-microbial activity of anti-tubercular drugs [6,10,11]. Unlike other fast-growing mycobacteria, such as *Mycobacterium smegmatis*, *M. aurum* has the ability to survive within macrophages [12,13] and has been used for high throughput intracellular drug screening, allowing assessment of the ability of compounds to permeate the cell membrane and their stability within the cell [14,15]. The emergence of strains of *M. tuberculosis* resistant to multiple first- and second-line drugs threatens efforts to control tuberculosis (TB) and has renewed interest in the search for new anti-tubercular agents [16]. Rapid-growing models for screening putative anti-tubercular compounds are needed to accelerate drug discovery studies. Similarly, surrogate bacteria are needed to enable studies on drugs that may improve treatment for infection with non-culturable *Mycobacterium leprae*. Knowledge of the bacterial genome could enhance understanding of the molecular basis for drug resistance, and to this end, the genome of *M. aurum* has been sequenced and annotated. The genome was placed in a mycobacterium phylogeny, and comparisons with *M. tuberculosis*, *M. leprae* and *M. smegmatis* genomes were made in relation to susceptibility towards anti-tubercular drugs.

Materials and methods

M. aurum sample and DNA extraction

The *M. aurum* (NCTC 10437) was grown in 7H9 Middlebrook broth (Becton Dickinson, USA) supplemented with 10% albumin–dextrose–catalase (ADC) at 35 °C. DNA was extracted using the Biltoven RFLP protocol [17]. In brief, log phase growth bacteria were treated with lysozyme, sodium dodecyl sulphate, proteinase K, N-cetyl-N,N,N-trimethyl ammonium bromide (CTAB) and chloroform-isoamyl alcohol prior to precipitation with isopropanol. Minimum inhibitory concentration (MIC) values for ethambutol, isoniazid, pyrazinamide and rifampicin drugs for the same *M. aurum* strain are available [18]. Duplications in *M. aurum* of *embB* and *katG* loci were confirmed by Sanger sequencing. For details of primers used, see Supplementary Table 1.

DNA sequencing and genome assembly

The *M. aurum* genomic DNA was sequenced using a 101 bp paired-end library on the Illumina HiSeq2000 platform. The

raw sequence data (size 0.55 Gb, ~5.5 million paired reads, available from ENA ERP009288, minimum base call accuracy greater than 99%) underwent *de novo* assembly using SPAdes software [19]. The SSPACE software [20] was applied to scaffold the assembly, and a combination of IMAGE [21] and GapFiller [22] routines were used to further close or reduce the length of remaining gaps. An alternative approach using Velvet assembly software [23] led to a near identical assembly. Genomic annotation was transferred to the draft genome using the Prokka pipeline [24]. The pipeline searches for genes present in contigs and compares them with protein and DNA databases to annotate them. The *cd-hit* software [25,26] was used to integrate the annotation from 8 mycobacterial species to create a non-redundant blast “primary” database used by the Prokka pipeline. To validate the draft assembly and annotation pipeline, the transferred annotation was compared against the *kas* operon sequence (GenBank: DQ268649.2). All 5 genes from the GenBank entry (*fabD*, *acpM*, *kasA*, *kasB*, *accD6*) were annotated in the correct order and orientation in the assembly.

Comparative genomics

Genomes from 27 species used in whole genome comparisons were downloaded from *ensembl* (bacteria.ensembl.org), and the Uniprot taxon identification numbers are listed in Table 1. Gene multiple alignments were constructed using *clustalw2* [27] for 16S rRNA and *MACSE* software [28] for *rpoB* sequences. *Raxml* software [29] was used to construct the best scoring maximum likelihood tree, which was rooted using the *Corynebacterium glutamicum* (strain: ATCC 13032) reference sequence, an organism closely related to the mycobacterium genus [30]. Pairwise gene alignments were constructed using *MACSE* software, which uses the translated amino acid sequence and accounts for frame shifts and premature stop codons. Sequence identities were calculated using the SIAS webserver. Gaps were not used in the calculation of the percent identity. Whole genome alignments were constructed using *mercator* and *mauid* programs [31], and the resulting homology map was inspected and drawn using *CIRCOS* [32]. Orthologue clusters were created using *OrthoMCL* [33]. To identify any protein coding genes under selective pressure across *M. aurum*, *M. tuberculosis*, *Mycobacterium bovis* – BCG, *M. smegmatis*, and *M. leprae*, the *Ka/Ks* ratio was calculated, where *Ka* is the number of non-synonymous substitutions per non-synonymous site, and *Ks* is the number of synonymous substitutions per synonymous site. Ratio values less than one imply stabilizing or purifying selection, whilst values greater than one imply positive selection. To measure the degree of polymorphism across the genes, the nucleotide diversity (π) was also calculated using the same mycobacterial sample alignments. The *Ka/Ks* and π metrics were calculated using *variscan* (<http://www.ub.edu/softevol/variscan>) and *PAML* (<http://abacus.gene.ucl.ac.uk/software/paml.html>) software, respectively.

Table 1 – Genomic characteristics of *M. aurum* in the context of related species.

Organism	Chromosome accession number	Uniprot Strain taxon id	Assembled genome (bp)	G + C content	No. genes	Relative in vitro growth rate	ACDP risk class ^a
<i>M. leprae</i>	AL450380.1	272631	3268203	57.80	1605	Unculturable	3
<i>C. glutamicum</i>	HE802067.1	1204414	3309401	53.81	3099	Rapid	1
<i>M. bovis</i>	BX248333	233413	4345492	65.63	3952	Slow	3
<i>M. tuberculosis</i>	AL123456.3	83332	4411532	65.61	4047	Slow	3
<i>M. xenopi</i>	AJFI01000000	1150591	4434836	66.11	4281	Slow	2
<i>M. canetti</i>	HE572590.1	1048245	4482059	65.62	3981	Slow	3
<i>M. thermoresistibile</i>	AGVE01000000	1078020	4870742	69.02	4614	Rapid	1
<i>M. hassiacum</i>	AMRA01000000	1122247	5000164	69.46	4959	Rapid	1
<i>M. abscessus</i>	CU458896.1	36809	5067172	64.15	4942	Rapid	1
<i>M. intracellulare</i>	CP003322.1	487521	5402402	68.10	5144	Slow	2
<i>M. neoaurum</i>	CP006936.1	700508	5438192	66.88	4217	Rapid	1
<i>M. avium</i>	CP000479.1	243243	5475491	68.99	5120	Slow	2
<i>M. gilvum</i>	CP002385.1	278137	5547747	67.86	5349	Rapid	1
<i>M. colombiense</i>	AFVW02000000	1041522	5579559	68.09	5197	Slow	1
<i>M. indicus pranii</i>	CP002275.1	1232724	5589007	68.03	5254	Rapid	1
<i>M. ulcerans</i>	CP000325.1	362242	5631606	65.47	4160	Slow	3
<i>M. yongonense</i>	CP003347.1	1138871	5662088	67.90	5390	Slow	1
<i>M. phlei</i>	AJFJ01000000	1150599	5681954	69.21	5435	Rapid	1
<i>M. aurum</i>	TBA^b	TBA	6019822	67.52	5684	Rapid	1
<i>M. vaccae</i>	ALQA01000000	1194972	6245372	68.60	5949	Rapid	1
<i>M. chubuense</i>	CP003053.1	710421	6342624	68.29	5843	Rapid	1
<i>M. fortuitum</i>	ALQB01000000	1214102	6349738	66.21	6241	Rapid	2
<i>M. vanbaalenii</i>	CP000511.1	350058	6491865	67.79	5979	Rapid	1
<i>M. parascrofulaceum</i>	ADNV01000000	525368	6564171	68.45	6456	Slow	1
<i>M. kansasii</i>	CP006835.1	557599	6577228	66.23	5866	Slow	2
<i>M. marinum</i>	CP000854.1	216594	6636827	65.73	5452	Slow	2
<i>M. smegmatis</i>	CP000480.1	246196	6988209	67.40	6938	Rapid	1
<i>M. rhodesiae</i>	AGIQ01000000	931627	7281599	66.07	7024	Rapid	1

^a UK Advisory Committee on Dangerous Pathogens (ACDP) <http://www.hse.gov.uk/pubns/misc208.pdf>.

^b ENA number ERP009288.

Results

The *M. aurum* genome

A total of ~5.5 million high quality paired end (101 bp) reads were used to assemble the *M. aurum* genome. The final *M. aurum* assembly consisted of 46 contigs, 43 of which were over 500 bp in length. The median contig length (N50) was 265 Kb (minimum 315 bp, maximum 742,983 bp). The total genome length (~6.02 Mb, G + C content 67.52%) is longer than *M. tuberculosis* (4.4 Mbp) and *Mycobacterium canettii* (4.5 Mbp), but shorter than *Mycobacterium marinum* (6.6 Mbp) and *M. smegmatis* (7.0 Mbp) (Table 1). A total of 5684 coding sequences, 1 tmRNA, 4 rRNA and 51 tRNA features were annotated, and of these 4306 (75%) were assigned a function (Fig. 1). The final contigs and annotation are available for download (pathogenseq.lshtm.ac.uk/m_aurum).

M. aurum and the mycobacteria phylogeny

A phylogenetic analysis using 27 mycobacterial whole genome sequences revealed that *M. aurum* clustered with *Mycobacterium vaccae* and *Mycobacterium vanbaalenii* within a clade related to fast-growing mycobacteria (Fig. 2). Slow-growing bacteria, including *M. tuberculosis*, clustered within

a distinct clade. However, *Mycobacterium indicus pranii*, a fast-growing mycobacterium and immunotherapy and vaccine candidate for leprosy and tuberculosis [34], clustered within the slow-growing clade. The very high bootstrap support values for the phylogenetic tree (median 100%, range 77–100%) indicates the high precision afforded when using whole genome data. Previously, *hsp65*, *sodA*, *recA*, *rpoB* and 16S rRNA gene sequence data were used to barcode bacteria, with the latter approach being adopted widely [35]. The assembled 16S rRNA sequence for *M. aurum* had the highest identity with *M. vanbaalenii* (99%), *Mycobacterium rhodesiae* (99%), and *Mycobacterium austroafricanum* (99%), in concordance with previous reports [36,37]. The phylogenetic tree constructed using 16S rRNA sequences was broadly similar to that from whole genome data (Supplementary Fig. 1). However, *M. aurum* and *M. vanbaalenii* clustered closer to *Mycobacterium abscessus* rather than *Mycobacterium gilvum*, and the topology was less robust with lower bootstrap support values.

Comparison to the *M. tuberculosis* and *M. leprae* genomes

The *M. aurum* assembled contigs were ordered according to the *M. tuberculosis* H37Rv reference genome (AL123456.3), leading to 10 gapped scaffolds. Most of the *M. tuberculosis*

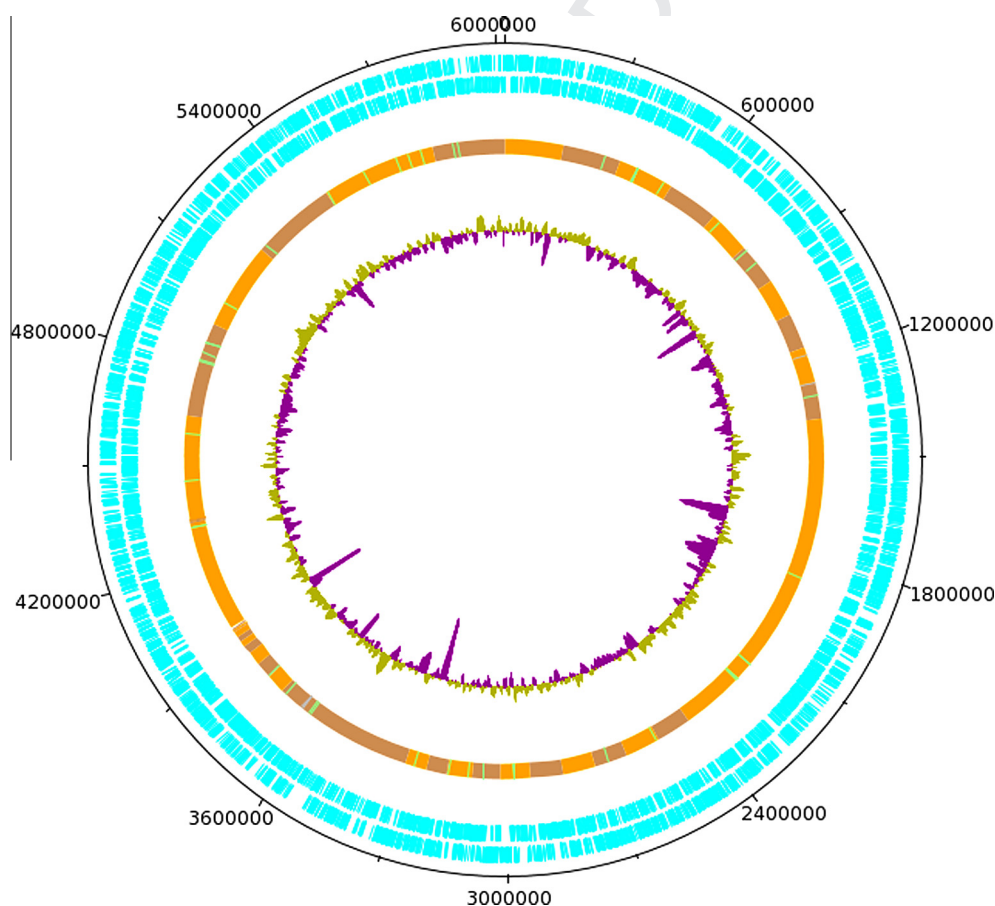


Fig. 1 – An annotated circular view of the *M. aurum* genome (length ~6.02 Mb). Innermost track: G + C% content; middle track: the 46 contigs, alternating between brown and orange with green and grey lines representing tRNA and rRNA, respectively; outer track: the 5684 forward and reverse genes.

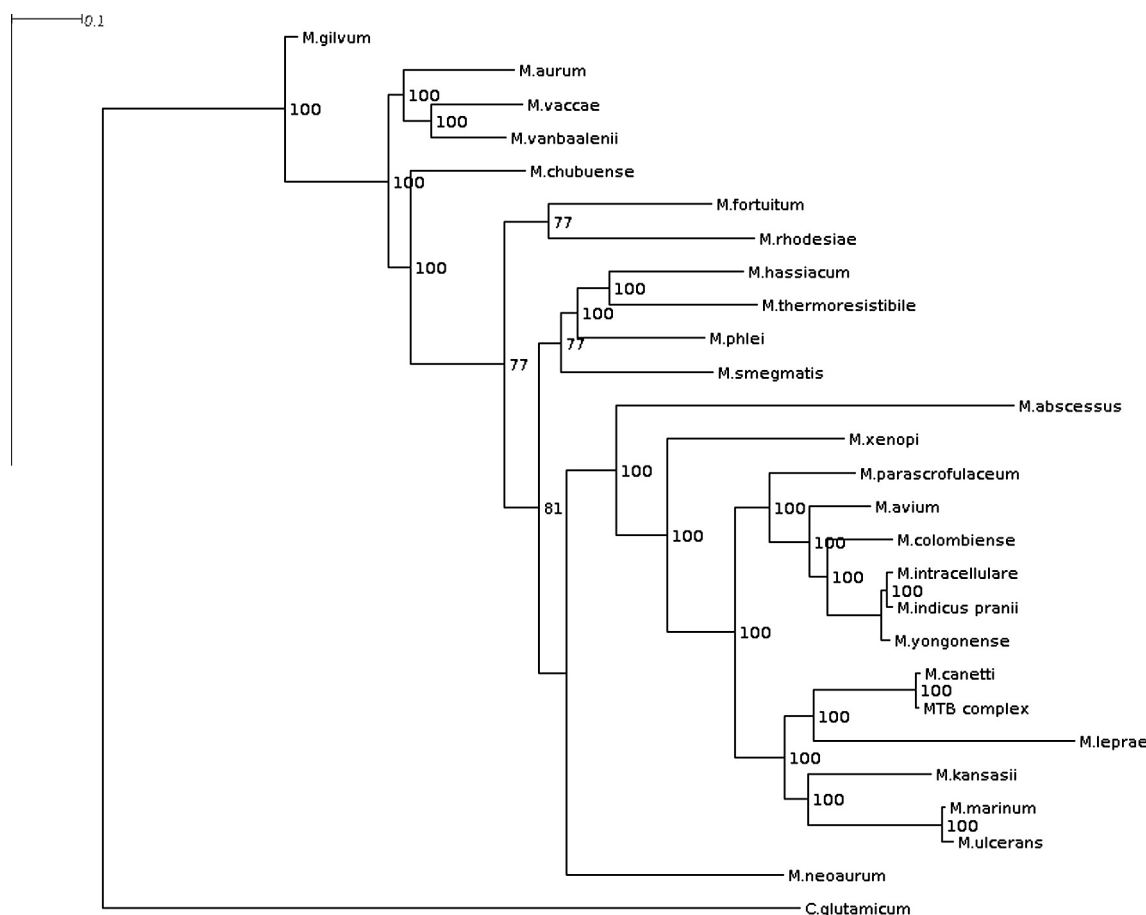


Fig. 2 – *M. aurum* and the mycobacterium phylogeny constructed using 27 whole genome reference sequences. *Constructed using RaXML and statistic support for lineages was based on 100 bootstrap samples. 27 reference sequences used are described in Table 1.

genome (86%) had regions with synteny in *M. aurum*. The map of homology between the 10 *M. aurum* scaffolds and the *M. tuberculosis* genome consisted of 67 regions of synteny (Supplementary Table 2 and Fig. 3a). Although there was high similarity between *M. aurum* and *M. tuberculosis*, there was evidence for large-scale rearrangements (Fig. 3a). Twenty-eight genes required for survival within macrophages were observed, but a further two (*lpqY* and *eccA₁*) could not be found [38] (Supplementary Table 3). The putative proteome for *M. aurum* suggests it lacks 1002 proteins present in *M. tuberculosis*, but has an additional 2090 proteins not seen in *M. tuberculosis* (see Table 2).

The map of homology between the 10 *M. aurum* scaffolds and the *M. leprae* genome consisted of 73 segments of synteny (Supplementary Table 2 and Fig. 3b). For *M. aurum* and *M. leprae* there were 2047 and 222 unique proteins, respectively, which had no orthologue in the other mycobacteria (see Supplementary Table 2). *M. smegmatis* is often used as a fast-growing model of *M. tuberculosis*. A similar analysis carried out between *M. tuberculosis* and *M. smegmatis* revealed 979 and 2314 unique proteins for each, respectively, which had no orthologue in the other mycobacteria. When compared with the *M. aurum*–*M. tuberculosis* analysis, the number of apparently unique proteins in *M. smegmatis* was higher by 224 proteins.

Drug resistance candidate genes

Pairwise alignments were constructed for the known drug target genes to establish the degree of homology between *M. aurum* and *M. tuberculosis* (Table 2). The sequence identity at the DNA level varied from 68.6% for *pncA* (pyrazinamide drug-related) to 96.2% for *rrs* (streptomycin, capreomycin). The percentage of amino acid identity was higher than the sequence identity, being high among all drug resistance candidate genes analysed (range 90.6–99.2%). Interestingly, two genes at different locations were annotated as *katG* in the *M. aurum* genome, and denoted as *katG1* and *katG2*. The percent identity between the two genes and their *M. tuberculosis* homologue at the DNA level are 73.6% and 68.8% (Supplementary Fig. 2). The putative *M. aurum* *katG1* found in contig 20 (*aurum03417*) demonstrated the highest homology to the *M. tuberculosis* *katG* gene (Rv1908c) and *M. smegmatis* MSMEG_6384. The second *M. aurum* *katG2* (*aurum 02416*) located in contig 2 (*katG2*) was most homologous with *M. smegmatis* MSMEG_3461. A third *M. smegmatis* gene, MSMEG_3729, showed weak homology to each of the *katG* genes in *M. aurum* and *M. tuberculosis*. Two copies of *embB*, a gene associated with ethambutol in *M. tuberculosis*, were also found in different locations in *M. aurum* (72.3% and 47.7% identity). The semi-identical duplications for each of *katG*

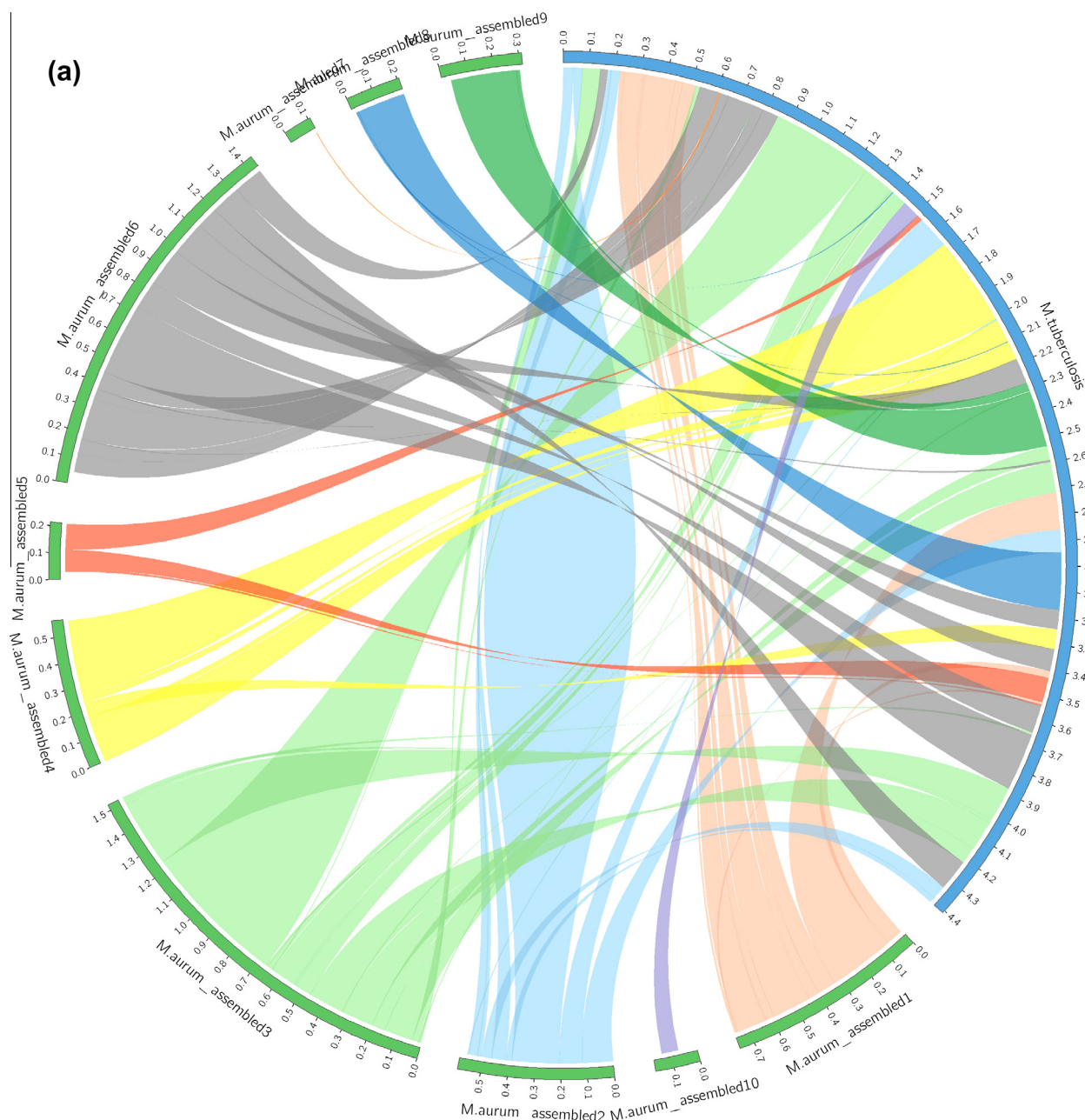


Fig. 3 – Homology between *M. aurum* and *M. tuberculosis* and *M. leprae*. (a) *M. aurum* (green) and *M. tuberculosis* H37Rv (blue). The ten contigs provide 67 segments of syntenicity with *M. tuberculosis* H37Rv. The segments range from 2,266 bp to 391,674 bp in length. (b) *M. aurum* (green) and *M. leprae* (blue). The ten contigs provide 73 segments of syntenicity with *M. leprae*. The segments range from 2,495 bp to 193,922 bp in length.

254 and *embB* were confirmed by PCR and Sanger sequencing
255 (Supplementary Table 4).

256 Across a range of therapeutic agents, potential differences
257 in minimum inhibitory concentration (MIC) levels between *M.*
258 *tuberculosis* (H37Rv) and *M. aurum* for isoniazid, ethambutol
259 and ofloxacin (Table 2) are available [8,18], with the biggest
260 difference for isoniazid. The MIC values for isoniazid were
261 greatest in *M. smegmatis* (2 mg/L), followed by *M. aurum* (0.4)
262 and *M. tuberculosis* (0.02–0.2). No known *M. tuberculosis* muta-
263 tions were identified in the *katG*, *inhA* (isoniazid), *ethA*, *ethR*
264 (ethambutol), and *gyrA/B* (ofloxacin) orthologues in *M. aurum*.

Homologues of *ahpC* and *embR* genes, associated with isoni-
azid and ethambutol drug resistance respectively, were not
observed in the *M. aurum* genome.

The alignments were compared across *M. aurum*, *M. tuber-*
tuberculosis, *M. bovis* – BCG, *M. smegmatis*, and *M. leprae* at the loci
considered drug targets or those loci considered to have
important functional roles (Table 3). All loci had a high per-
centage (~90%) of their nucleotides analyzable across the
mycobacteria, except *fas* and *gyrA* where there were large
insertions in *M. aurum* and *M. leprae*, respectively. Only three
loci did not have alignment gaps: *inhA* (isoniazid drug-

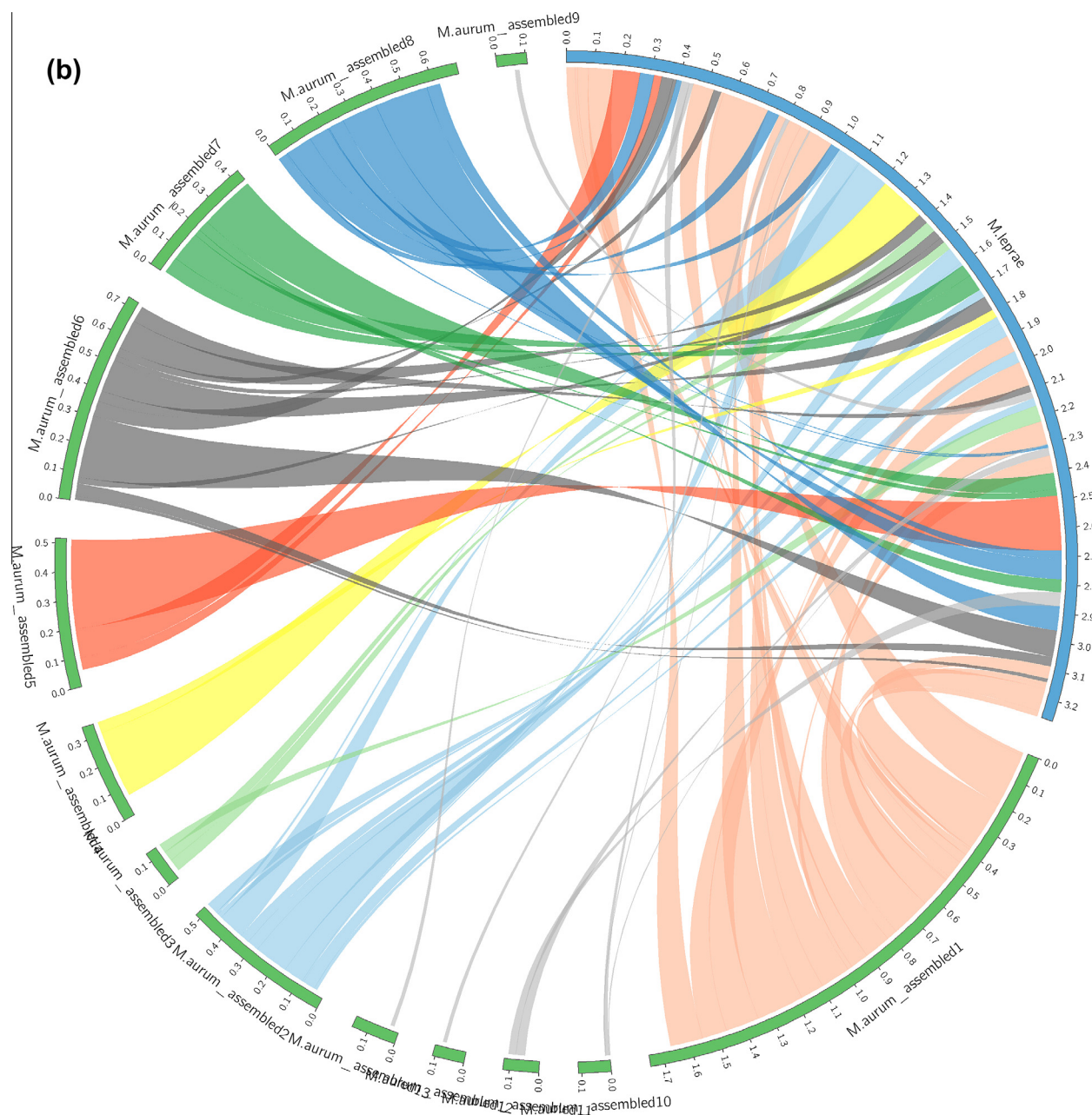


Fig 3. (continued)

276 related); *rpsL* (streptomycin); and *kasA* (thiolactomycin). The
277 *ddn* (delamanid), *fpo1* (para-aminosalicylic acid), *murC/D/E/F*
278 family (isoquinolines), and *nat* (cholesterol metabolism) loci
279 were the most polymorphic (>40% sites segregating, nucleotide
280 diversity $\pi > 0.2$). In contrast, the *rrs* gene associated with
281 streptomycin drug resistance was the most conserved (2.9%
282 segregating sites, pairwise diversity $\pi = 0.029$). In general,
283 there was a modest degree of conservation in most genes
284 (all with >50% of sequence conserved), which would be
285 expected given the known synergistic drug effects across
286 mycobacteria. All candidate genes reported *Ka/Ks* values
287 much lower than 1, consistent with the selective removal of
288 alleles that are deleterious (purifying selection). The highest
289 *Ka/Ks* value was observed for *nat* (Rv3566c), a gene encoding

arylamine acetylase that is associated with resistance to isoniazid [39].

Discussion

The draft genome sequence of *M. aurum* (length ~6.02 Mb, G + C content 67.52%) has been assembled. The genome assembly consists of 46 contigs and provides the first insight into the genetic code of *M. aurum*. Lack of alternative sequence data for this bacterium, particularly from technologies with longer reads, prevents closure of the gaps at this time. Using whole genome alignments, the placement of *M. aurum* within the mycobacterial phylogeny, close to *M. vaccae* and *M. vanbaalenii*, was confirmed. The analysis of loci

Table 2 – Drug minimum inhibitory concentrations (MICs) and candidate resistance gene identity between *M. aurum* and *M. tuberculosis* at drug resistance loci.

Drug	MIC ^b <i>M. aurum</i> mg/L (μM)	MIC ^b H37Rv mg/L (μM)	<i>M. tb</i> loci	Gene homology with <i>M. aurum</i> (%)	Protein similarity score (%)	<i>M. aurum</i> feature
Isoniazid	0.40 (3.65)	0.02–0.2 (0.15–1.46)	<i>katG</i> ^a	72.06	93.23	2 loci
			<i>inhA</i> ^a	87.40	98.14	Absent
			<i>ahpC</i>	–	–	
Rifampicin	0.10 (0.12)	0.10 (0.12)	<i>kasA</i>	86.33	99.04	
			<i>rpoB</i> ^a	90.74	97.62	
Ethambutol	0.5 (2.45)	0.47 (2.30)	<i>rpoC</i>	90.20	98.10	2 loci
			<i>embB</i>	69.87	91.46	
			<i>embA</i>	68.87	94.28	
			<i>embC</i>	73.83	93.78	
Streptomycin, aminoglycosides, capreomycin	0.2 (0.34) – –	0.1–0.5 (0.17–0.86) – –	<i>embR</i>	–	–	Absent
			<i>rrs</i>	–	–	
			<i>rpsL</i>	96.00	99.20	
Pyrazinamide	>100, (812.26)	>100 (812.26)	<i>tlyA</i>	73.58	92.98	
			<i>pncA</i>	64.17	90.62	
Ethionamide	5 (30.08)	0.6–2.5 (3.6–15.04)	<i>rpsA</i>	93.56	98.55	
			<i>ethA</i>	65.71	94.30	
Ofloxacin	0.2 (0.55)	1–2 (2.77–5.53)	<i>ethR</i>	69.15	93.11	
			<i>gyrA</i>	90.34	97.75	
			<i>gyrB</i>	86.39	92.30	

Homology as calculated using protein alignment. Protein similarity is quite high for most proteins analysed.

a Selected alignments can be found in http://pathogenseq.lshtm.ac.uk/m_aurum/.

b MIC value Ref. [18].

Table 3 – A comparison across *M. aurum*, *M. tuberculosis*, *M. bovis* – BCG, *M. smegmatis*, and *M. leprae* alignments at drug targets or other important loci.

Drug resistance or function	Gene name	Alignment length ^a	% Sites analysed ^b	Gaps	% Segregating sites	% Conserved sites	π ^c	Ka/Ks ^d
Bedaquiline (TMC207) BTZ043, DNB1, VI-9376, 377790, TCA1 Cholesterol metabolism	<i>atpE</i>	261	94.25	15	28.0	72.0	0.150	0.089
	<i>dprE1</i>	1410	98.09	27	34.6	65.4	0.210	0.128
	<i>hsaA</i>	1191	99.50	6	27.6	72.4	0.166	0.150
	<i>hsaB</i>	570	98.95	6	26.2	73.8	0.157	0.182
	<i>hsaC</i>	903	99.67	3	30.1	69.9	0.182	0.104
	<i>hsaD</i>	921	93.81	57	30.9	69.1	0.189	0.129
Fluoro-quinolones	<i>nat</i>	861	95.82	36	43.8	56.2	0.268	0.287
	<i>gyrA</i>	3807	65.33	1320	32.2	67.8	0.171	0.070
	<i>gyrB</i>	2157	93.88	132	36.2	63.8	0.193	0.077
Isoniazid/pyridomycin Isoquinolines	<i>inhA</i>	810	100	0	28.1	71.9	0.152	0.101
	<i>murC</i>	1512	94.64	81	43.1	56.9	0.235	0.170
	<i>murD</i>	1509	96.02	60	46.1	53.9	0.254	0.240
	<i>murE</i>	1653	91.83	135	48.1	51.9	0.267	0.228
	<i>murF</i>	1617	91.65	135	42.7	57.3	0.230	0.167
Isoxyl (thiocarlide) PA-824, delamanid (OPC67683) para-aminosalicylic acid	<i>fas</i>	10701	85.79	1521	37.0	63.0	0.195	0.163
	<i>ddn</i>	513	88.30	60	44.6	55.4	0.280	0.331
	<i>folP1</i>	882	92.18	69	42.9	57.1	0.241	0.144
Q203, IP3 Rifampicin Streptomycin	<i>folP2</i>	957	88.71	108	35.8	64.2	0.198	0.129
	<i>qcrB</i>	1695	96.46	60	31.5	68.5	0.174	0.126
	<i>rpoB</i>	3537	98.47	54	23.7	76.3	0.128	0.084
Thiolactomycin	<i>rpsL</i>	375	100	0	23.2	76.8	0.122	0.028
	<i>rrs</i>	1563	95.84	65	2.9	97.1	0.029	0.029
	<i>kasA</i>	1251	100	0	29.1	70.9	0.159	0.100
	<i>kasB</i>	1326	91.63	111	36.4	63.6	0.195	0.117

Selected alignments can be found at pathogenseq.lshtm.ac.uk/m_aurum/.

a The total number of columns in the alignment including gaps.

b A function of the number of sites used in determining the number of segregating and conserved sites.

c π nucleotide diversity.

d The Ka/Ks is the ratio of the number of non-synonymous substitutions per non-synonymous site (Ka) to the number of synonymous substitutions per synonymous site (Ks).

involved in drug resistance demonstrated homology with *M. tuberculosis* and *M. leprae*. This insight corroborates earlier investigations of *inhA* gene mutants of *M. aurum* that showed similarity in drug resistance mechanisms against isoniazid and ethionamide between *M. aurum* and *M. tuberculosis* [6,40]. The draft *M. aurum* genome is larger than that of *M. tuberculosis* with an additional 2090 genes not observed in *M. tuberculosis*; it is also lacking 1002 of the genes found in *M. tuberculosis*. Multiple copies of some homologous genes were observed. Of particular interest are two putative copies of *embB*, a gene involved in the biosynthesis of the mycobacterial cell wall component arabinan and that is associated with resistance to ethambutol in *M. tuberculosis*. Similarly, two annotated catalase-peroxidase (*katG*) genes that may be involved in the activation of the anti-tuberculosis pro-drug isoniazid were identified and confirmed. Multiple *katG* genes have been reported in other mycobacteria, for example in *Mycobacterium fortuitum* [41]. It could be hypothesized that the duplications of *katG* in *M. aurum* and *M. smegmatis* could have an effect on the MIC values. Further laboratory work is underway to elucidate the endogenous function of the observed duplications.

In summary, these genomic analyses support the use of *M. aurum* as a potential model organism for providing insights into *M. tuberculosis* biology, particularly for new drug development, with the possibility of leading to new control measures for tuberculosis disease. Further insight may be gained from the genome sequence of additional strains and related mycobacteria.

Conflicts of interest

The authors declare no conflict of interests.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.ijmyco.2015.05.001>.

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